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N-Terminus: 40
his gly the his Eye ter the tyr his tyr ser glu lys pro met ash tep glu ash sia
CAT GGA ACT CAC TET IGG ACT TAC CAT TAT TCT GAA AAG CCC ATG AAC TGG GAA AAT CCT arg lys phe Cyr lys gin san tyr the sep leu val ala ile gin asn lys arg giu ile AGA AMG TTC TCC AMG CAM MAT TAC ACA GAT TTA GTC GCC ATA CAA AMC AMG AGA GAA ATT glo tyr leu glu asn thr leu pro lys ser pro tyr tyr tyr trp ile gly ile arg lys GAG TAT TTA GAG AAT ACA TTG CCC AAA AGC CCT TAT TAC TAG ATA GGA ATC AGG AAA 110 gly lys met trp thr trp val gly thr ash lys thr leu thr lys glu sia glu ash ATT GGG AAA ATG TGG ACA TGG GTG GGA ACC LAG AAA ACT CTC ACT AAA GAA GCA GAG AAC 170 trp gly sle gly glu pro aen een lys lys eer lys glu aep [CYP] val glu ile tyr ile Too GoT CCT Coo GAG CCC AAC AAC AAG AAG TCC AAG GAG GAC [TCT] GTC GAG ATC TAT ATC leu Eye tyr the ale ser Eye gin pro giy ser Eye asn gly arg gly giu Eye vai glu cre rec tac ACA occ ter tes cac cca cca fer tes ACA occ ter tes cac cca cca cac aca fer tes cac the ile sea sen his this eye lie says ale gly tyr tyr gly pro gin sys gin tyr are and har cac accorded are time day sec of the tar are and har cac accorded are time say sec. acc ray tar tac see eec cas test cas tar leu gly man phe sen phe gin ser lys Eys ala phe man Eys ac glu erg glu leu TTG GGA AAC TTC ACC TTC CAG TCC AAG TETI CCT TTC AAC ISST TCT GAG GGA AGA GAG CTA leu gly thr sla glu thr gin CYA gly ala ser gly man trp ser pro glu pro ile CTT GGG ACT GCA GAA ACA CAG TGT GGA GCA TCT GGA AAC TGG TCA TCT CCA GAG CCA ATC CYA gin val val gin CYA giu pro leu giu ela pro giu leu giy thr met asp CYA ile TGC CAA GTG GTC CAG TGT GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC TGC ATC 280

his pro leu gly san phe seri phe gln ser lye Gys ale phe sen Gys seri glu gly arg CAC CCC TTG GGA AAAC TTG AGG TTG CAG TCC AAG TGT GCT TTG AAC TGT TCT GAG GGA AGA glu leu leu gly thr als glu thr gln [cys] gly als ser gly ash tip sel ser pro glu GAG CTA CTT GGG ACT GGA GAA ACA CAG [TC] GGA GCA TCT GGA AACT TGG TCA TCT CCA GAG TTTTACACGCAGGCATCTCCCCACATTAGAGATGCAGTGTTTGCTCAACGAATCTGGAAGGATTTCTTCATGACCA TECCENTETECTTTTCCTAGGAGAATAATTCCACACACTGCACCCCATGATGGCCACCAAACATCAAAGAAGGCAAAA TGCATTGAGTTTTAGTTTTGAGTTTTCCCTTCTCTTTATTAGATCTCTGATGGTTCCTTGAAGTCAGTGTTCT TATTAATAGTTAATGATAACACAACCCACTCTCTTGGAGCTGATGTTATGAAGACAACAGGTAGAAAAATTC itcaggetggagtgaeaccettttctttccetaacatettctactagataectaaatttaagattcaggaca GCTGTCCCCAACTCTTACCATGTCTTTTATAACTTGCTCCTTAACTTGCCCAACCTGTAGGCTATCTCATTTTCTCCC

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'GTNKTLTKEAENWGAGEPNNKKSKTOCVEIYIKAEADSGKWNDDACHKA MI FPWRGEGTY WGS ANILK LWVWTLL CODFLI HHGTHCWTYHYSEKPMNIMI FRUWKGOSTOADL WNIFKLWGWTML CCOFLAHHGTYCWTYHYSEKPMNI | Man Cytascop ws CsG HGE CV EI I NN H T C I CD A G Y Y G P G C G V V G C E P L K A A L C Y T A S C O P w S C S G H G E C V E I I NN H T C I C D A G Y Y G P G C G V V G C E P L ENARKFCKONYTOLVAIONKREIEYKENTLPKSPYYYWIGIRKIGKMWT EAPELGTMDCI HPLGNFSFOSKCAFNCSEGRELLGTAETOCGASGNWSSP EAPELGTMDCTHPFGNFSFSSOCAFSCSEGTNLTGI EETTCGPFGNWSSP EPI COVVOCEPLEAPELGTMOCI HPLGNFSFOSKGAFNCSEGRELLGTAE Transmembrane Domain TOCGASGNWSSPEPICOETNRSFSKIKEGDYNPEF! PVAVMVTAFSGLAF TIGESSGIWSNPSPICOKLDKSFSMIKEGDYNPLFIPVAVMVTAFSGLAF Complement Binding Repeat 1 Complement Binding Repeat 2 Lectin Domain Signal Sequence _> MLHR HLHR MLHR MLHK HLHR MLHR HLHR ALHR HLHR MLHR HLHR M.HR

Cytoplasmic Domain —

HLHR |

n.

MLHR I WLARRLKKGKKSOERMDDPY HLHR I WLARRLKKGKKSKRSMNOPY

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MW (Kd) —— 200 —— 116 —— 93

---- 66

----- 45

Fig. 4A

Fig. 4 B

K M KF K V<u>VIL</u> K
10 20 30
EKPMNWENARKFXKQNYTDLVAIQNKXXIEYL

Fig. 4c

A C A C A C AAG CCC ATG AAT TGG GAG AAT GC 3'

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A B C D E F MW (Kd)

- 200

- 97

- 68

13

Fig. 6

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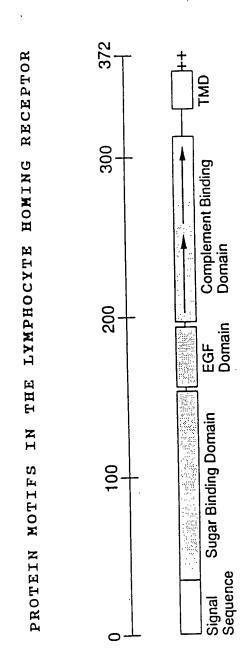
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> Notch S.purp. Pro.Z Fact.X Fact.VII Fact.IX Lin-12 Fact.XII

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HUC2 HUC3 HUB HUC4b HUC4b HUC4b HUC4b HUC4b HUC6mH HUBeta HUC2 HUB HUC2 HUB HUC2 HUB HUC6mH HUC4b HUC6mH HUC
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